

OIPE

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/10/017,621

TIME: 09:56:48

Input Set : A:\RTS-0350 Sequence Listing.txt

Output Set: N:\CRF3\01042002\J017621.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Susan M. Freier
 4 Mark P. Roach
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
 8 <130> FILE REFERENCE: RTS-0350
 10 <140> CURRENT APPLICATION NUMBER: US/10/017,621
 10 <141> CURRENT FILING DATE: 2001-12-07
 10 <160> NUMBER OF SEQ ID NOS: 89
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 20
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctccctcaggg 20
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 20
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 33 <223> OTHER INFORMATION: Antisense Oligonucleotide
 35 <400> SEQUENCE: 2
 36 atgcattctg cccccaagga 20
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 1745
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Homo sapiens
 44 ~~<220> FEATURE:~~
 46 <220> FEATURE:
 47 <221> NAME/KEY: CDS
 48 <222> LOCATION: (124)...(1614)
 50 <400> SEQUENCE: 3
 51 tggaagcagc gtaaaggatg gacaggaatg cagaggtagg caggaggacc agcagtgtga 60
 53 ctgctgaaac ccaggggagg gccccgcggc tctgaggttg ctgcgcgcgc cccgccgata 120
 55 gcc atg gat cgg atg aag aag atc aaa cgg cag ctg tca atg aca ctc 168
 56 Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met Thr Leu
 57 1 5 10 15
 59 cga ggt ggc cga ggc ata gac aag acc aat ggt gcc cct gag cag ata 216
 60 Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln Ile
 61 20 25 30
 63 ggc ctg gat gag agt ggt ggt ggt ggc ggc agt gac cct gga gag gcc 264
 64 Gly Leu Asp Glu Ser Gly Gly Gly Gly Ser Asp Pro Gly Glu Ala
 65 35 40 45
 67 ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc cca ctc 312
 68 Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro Leu
 69 50 55 60
 71 agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg tct gat 360

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72 Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser Asp
73      65      70      75
75 ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg cag tct      408
76 Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln Ser
77 80      85      90      95
79 cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc tcc act      456
80 Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser Thr
81      100      105      110
83 gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg ctg cct      504
84 Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu Pro
85      115      120      125
87 gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt gac aag      552
88 Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp Lys
89      130      135      140
91 ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att ggc ttt      600
92 Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly Phe
93      145      150      155
95 ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag ggt acc      648
96 Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly Thr
97 160      165      170      175
99 tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac ctt gtg      696
100 Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu Val
101      180      185      190
103 gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc tgc acc      744
104 Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr
105      195      200      205
107 gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc aac atc      792
108 Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala Asn Ile
109      210      215      220
111 gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc ctt gtc      840
112 Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr Leu Val
113      225      230      235
115 ttt gag tac ctg gac aag gac ctg aag cag tac ctg gat gac tgt ggg      888
116 Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp Cys Gly
117 240      245      250      255
119 aac atc atc aac atg cac aac gtg aaa ctg ttc ctg ttc cag ctg ctc      936
120 Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu Leu
121      260      265      270
123 cgt ggc ctg gcc tac tgc cac cgg cag aag gtg cta cac cga gac ctc      984
124 Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp Leu
125      275      280      285
127 aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag ctg gct      1032
128 Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
129      290      295      300
131 gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca tac tcc      1080
132 Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr Tyr Ser
133      305      310      315
135 aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg ctt ggg      1128
136 Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu Leu Gly

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137 320          325          330          335
139 tcc acg gac tac tcc act cag att gac atg tgg ggt gtg ggc tgc atc 1176
140 Ser Thr Asp Tyr Ser Thr Gln Ile Asp Met Trp Gly Val Gly Cys Ile
141          340          345          350
143 ttc tat gag atg gcc aca ggc cgt ccc ctc ttt ccg ggc tcc acg gtg 1224
144 Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr Val
145          355          360          365
147 gag gaa cag cta cac ttc atc ttc cgt atc tta gga acc cca act gag 1272
148 Glu Glu Gln Leu His Phe Ile Phe Arg Ile Leu Gly Thr Pro Thr Glu
149          370          375          380
151 gag acg tgg cca ggc atc ctg tcc aac gag gag ttc aag aca tac aac 1320
152 Glu Thr Trp Pro Gly Ile Leu Ser Asn Glu Glu Phe Lys Thr Tyr Asn
153          385          390          395
155 tac ccc aag tac cga gcc gag gcc ctt ttg agc cac gca ccc cga ctt 1368
156 Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro Arg Leu
157 400          405          410          415
159 gat agc gac ggg gcc gac ctc ctc acc aag ctg ttg cag ttt gag ggt 1416
160 Asp Ser Asp Gly Ala Asp Leu Leu Thr Lys Leu Leu Gln Phe Glu Gly
161          420          425          430
163 cga aat cgg atc tcc gca gag gat gcc atg aaa cat cca ttc ttc ctc 1464
164 Arg Asn Arg Ile Ser Ala Glu Asp Ala Met Lys His Pro Phe Phe Leu
165          435          440          445
167 agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc ata ttt 1512
168 Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser Ile Phe
169          450          455          460
171 gca cta aag gag att cag cta caa aag gag gcc agc ctt cgg tct tcg 1560
172 Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg Ser Ser
173          465          470          475
175 tcg atg cct gac tca ggc agg cca gct ttc cgc gtg gtg gac acc gag 1608
176 Ser Met Pro Asp Ser Gly Arg Pro Ala Phe Arg Val Val Asp Thr Glu
177 480          485          490          495
179 ttc taä gccacagacc gaggccccag caggcagcgg ctggagggat gccacacccc 1664
180 Phe
183 tcacagggca gcccceaact acatcttccc tgcttactct ctgcctacct gcctgagcca 1724
185 tggttacctg cccacttgtc c 1745
188 <210> SEQ ID NO: 4
189 <211> LENGTH: 15
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
195 <223> OTHER INFORMATION: PCR Primer
197 <400> SEQUENCE: 4
198 aggttgctcg cgcgc 15
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 22
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
208 <223> OTHER INFORMATION: PCR Primer

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210 <400> SEQUENCE: 5
211 acagctgccg tttgatcttc tt
214 <210> SEQ ID NO: 6
215 <211> LENGTH: 19
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
221 <223> OTHER INFORMATION: PCR Probe
223 <400> SEQUENCE: 6
224 cccgccgatc gccatggat
227 <210> SEQ ID NO: 7
228 <211> LENGTH: 19
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
234 <223> OTHER INFORMATION: PCR Primer
236 <400> SEQUENCE: 7
237 gaaggtgaag gtcggagtc
240 <210> SEQ ID NO: 8
241 <211> LENGTH: 20
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
247 <223> OTHER INFORMATION: PCR Primer
249 <400> SEQUENCE: 8
250 gaagatggtg atgggatttc
253 <210> SEQ ID NO: 9
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
260 <223> OTHER INFORMATION: PCR Probe
262 <400> SEQUENCE: 9
263 caagcttccc gttctcagcc
266 <210> SEQ ID NO: 10
267 <211> LENGTH: 20
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
273 <223> OTHER INFORMATION: Antisense Oligonucleotide
275 <400> SEQUENCE: 10
276 ctgtccatcc tttacgctgc
279 <210> SEQ ID NO: 11
280 <211> LENGTH: 20
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
286 <223> OTHER INFORMATION: Antisense Oligonucleotide
288 <400> SEQUENCE: 11

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289 ctgcattcct gtccatcctt                20
292 <210> SEQ ID NO: 12
293 <211> LENGTH: 20
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
299 <223> OTHER INFORMATION: Antisense Oligonucleotide
301 <400> SEQUENCE: 12
302 ctcctgccta cctctgcatt                20
305 <210> SEQ ID NO: 13
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
312 <223> OTHER INFORMATION: Antisense Oligonucleotide
314 <400> SEQUENCE: 13
315 gctggtcctc ctgcctacct                20
318 <210> SEQ ID NO: 14
319 <211> LENGTH: 20
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
325 <223> OTHER INFORMATION: Antisense Oligonucleotide
327 <400> SEQUENCE: 14
328 tcagcagtca cactgctggt                20
331 <210> SEQ ID NO: 15
332 <211> LENGTH: 20
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
338 <223> OTHER INFORMATION: Antisense Oligonucleotide
340 <400> SEQUENCE: 15
341 cctgggtttc agcagtcaca                20
344 <210> SEQ ID NO: 16
345 <211> LENGTH: 20
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
351 <223> OTHER INFORMATION: Antisense Oligonucleotide
353 <400> SEQUENCE: 16
354 tcatccgatc catggcgatc                20
357 <210> SEQ ID NO: 17
358 <211> LENGTH: 20
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
364 <223> OTHER INFORMATION: Antisense Oligonucleotide
366 <400> SEQUENCE: 17
367 ttgatcttct tcatccgatc                20

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VERIFICATION SUMMARY

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Input Set : A:\RTS-0350 Sequence Listing.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date